SEQUENCE LISTING

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<110> FUJII, et al., Tadashi

<120> Gene participating in the production of homoglutamic
acid and its use

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<150> JP10/232382
<151> 1998-08-05

<150> JP11/182362
<151> 1999-06-28

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<170> PatentIn Ver. 2.0

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ttgagcagat cgcactgcc atttgtagtg cgttaacggt tacaactaac actagacaca 780

atcagcacgg attcagcatg tcc ctt ctt gcc ccg ctc gcc ccg ctc cgc gcc 833
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cat gcc ggc acc cgc ctt acc cag ggc ctg tct gac ccg cag gtc gag 881
His Ala Gly Thr Arg Leu Thr Gln Gly Leu Ser Asp Pro Gln Val Glu
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cag ctg gcc gcc aac cac cct gac ctg cgc gcc gcc atc gac gcc gct 929
Gln Leu Ala Ala Asn His Pro Asp Leu Arg Ala Ala Ile Asp Ala Ala
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gcc gac gaa tac gcg cgc atc aaa ccg cag gcc gcg gca ttg ctg gac 977
Ala Asp Glu Tyr Ala Arg Ile Lys Pro Gln Ala Ala Ala Leu Leu Asp
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ctg gat gaa agc gcg cag atc gcc gcc gtg cag gat ggc ttc gtc aac 1025
Leu Asp Glu Ser Ala Gln Ile Ala Ala Val Gln Asp Gly Phe Val Asn
60   65   70   75

ttc tat gcc gat gat gcg gtg gtg ccc tat atc gcc ctg gcc gcc cgc 1073
Phe Tyr Ala Asp Asp Ala Val Val Pro Tyr Ile Ala Leu Ala Ala Arg
              80   85   90

2

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ggc tac ggc atg ctc ggc ttc ggc cat acc ccg gcc gat atc ctg gag      1169
Gly Tyr Gly Met Leu Gly Phe Gly His Thr Pro Ala Asp Ile Leu Glu
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gcg gtc ggc aag ccg cag gtg atg gcc aac atc atg act ccc tcg ctg      1217
Ala Val Gly Lys Pro Gln Val Met Ala Asn Ile Met Thr Pro Ser Leu
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gcc cag ggc cgc ttc att gcc gca atg cgc cgc gaa atc ggc cat acc      1265
Ala Gln Gly Arg Phe Ile Ala Ala Met Arg Arg Glu Ile Gly His Thr
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Arg Gly Gly Cys Pro Phe Ser His Phe Met Cys Leu Asn Ser Gly Ser
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Glu Ala Val Gly Leu Ala Ala Arg Ile Ala Asp Ile Asn Ala Lys Leu
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atg acc gac ccg ggc gcc cgg cat gcc ggc gcc acg atc aag cgc gtg      1409
Met Thr Asp Pro Gly Ala Arg His Ala Gly Ala Thr Ile Lys Arg Val
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Val Ile Lys Gly Ser Phe His Gly Arg Thr Asp Arg Pro Ala Leu Tyr
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tcc gat tcc acc cgc aag gcc tac gat gcg cat ctg gcc agc tac cgc      1505
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3

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gtg ttc ctg gag ccg gtg atg ggc gaa ggc gac ccg ggc cgt gcg gtg   1649
Val Phe Leu Glu Pro Val Met Gly Glu Gly Asp Pro Gly Arg Ala Val
            270                 275                 280

ccg gtg gac ttc tac cgc ctg gcc cgt gag ctg acc cgc gaa cac ggc   1697
Pro Val Asp Phe Tyr Arg Leu Ala Arg Glu Leu Thr Arg Glu His Gly
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agc ctg ctg ctg atc gat tcg atc cag gcc gcg ctg cgc gtg cac ggc   1745
Ser Leu Leu Leu Ile Asp Ser Ile Gln Ala Ala Leu Arg Val His Gly
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acc ctg tcc ttc gtc gac tac ccc ggc cac cag gag ctg gag gca ccg   1793
Thr Leu Ser Phe Val Asp Tyr Pro Gly His Gln Glu Leu Glu Ala Pro
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gac atg gag acc tac tcc aag gcc ctg aac ggc gcc cag ttc ccg ctg   1841
Asp Met Glu Thr Tyr Ser Lys Ala Leu Asn Gly Ala Gln Phe Pro Leu
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Ser Val Val Ala Val Thr Glu His Ala Ala Ala Leu Tyr Arg Lys Gly
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gtg tac ggc aac acc atg acc acc aac ccg cgg gcg ctg gac gtg gcc   1937
Val Tyr Gly Asn Thr Met Thr Thr Asn Pro Arg Ala Leu Asp Val Ala
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tgc gcc acc ctg gca cgc ctg gat gag ccg gtc cgc aac aat atc cgc   1985
Cys Ala Thr Leu Ala Arg Leu Asp Glu Pro Val Arg Asn Asn Ile Arg
380                 385                 390                 395

ctg cgt ggc cag cag gcg atg cag aag ctg gaa gca ttg aag gaa cgg   2033
Leu Arg Gly Gln Gln Ala Met Gln Lys Leu Glu Ala Leu Lys Glu Arg
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4

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ctg ggg ggc gcg atc acc aag gtg cag ggc acc ggc ctg ctg ttc tcc    2081
Leu Gly Gly Ala Ile Thr Lys Val Gln Gly Thr Gly Leu Leu Phe Ser
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tgc gag ctg gcc ccg cag tac aag tgc tac ggg gcc ggc tcc acc gag    2129
Cys Glu Leu Ala Pro Gln Tyr Lys Cys Tyr Gly Ala Gly Ser Thr Glu
            430                 435                 440


gag tgg ctg cgc atg cac ggg gtc aat gtg atc cac ggc ggc gag aat    2177
Glu Trp Leu Arg Met His Gly Val Asn Val Ile His Gly Gly Glu Asn
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tcg ctg cgc ttc acc ccg cac ttc ggc atg gac gag gcc gaa ctg gac    2225
Ser Leu Arg Phe Thr Pro His Phe Gly Met Asp Glu Ala Glu Leu Asp
    460                 465                 470                 475


ctg ctg gtg gag atg gtc ggg cgt gcg ctg gtc gaa ggc cca cgc cgg    2273
Leu Leu Val Glu Met Val Gly Arg Ala Leu Val Glu Gly Pro Arg Arg
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gcc tga tccgcacccg caggacggaa ggcacgagcc caccgtgagg cgggctcttt gc 2331
Ala Stop


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7

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Ala Leu Gly Leu Asp Ala Thr Asn Ser Gly Thr Tyr Leu Gly Asp Gly
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gaa tgg tcc agc gct acc ggt gcc ggg acc atc agc ccg cgc aac ccg   2971
Glu Trp Ser Ser Ala Thr Gly Ala Gly Thr Ile Ser Pro Arg Asn Pro
        25              30                  35

acc acc ggc gag gtc att gcc cag gtc cag gcc acc acc gag gcg gac   3019
Thr Thr Gly Glu Val Ile Ala Gln Val Gln Ala Thr Thr Glu Ala Asp
40                  45                  50                  55

tac gaa acc atc ctg gcc cgc gcc cag cag gcc ttc aag gtc tgg cgc   3067
Tyr Glu Thr Ile Leu Ala Arg Ala Gln Gln Ala Phe Lys Val Trp Arg
                    60              65                  70

acc acc ccg gca ccg cgc cgc ggc gag gcc atc cgc ctg tgt ggc gag   3115
Thr Thr Pro Ala Pro Arg Arg Gly Glu Ala Ile Arg Leu Cys Gly Glu
            75              80                  85
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8

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gcc ctg cgc cgc cac aag gac gcg ctg ggt tcg ctg gtc gcg ctg gaa        3163
Ala Leu Arg Arg His Lys Asp Ala Leu Gly Ser Leu Val Ala Leu Glu
        90              95                  100

atg ggc aag tcc aag ccg gaa ggc gac ggc gaa gtc cag gaa atg atc        3211
Met Gly Lys Ser Lys Pro Glu Gly Asp Gly Glu Val Gln Glu Met Ile
        105             110                 115

gac atc gcc gac ttt gcc gtc ggc cag agc cgc atg ctg tat ggc tac        3259
Asp Ile Ala Asp Phe Ala Val Gly Gln Ser Arg Met Leu Tyr Gly Tyr
120             125                 130                 135

acc atg cac agc gag cgc ccc ggc cac cgc atg tac gag cag tac cag        3307
Thr Met His Ser Glu Arg Pro Gly His Arg Met Tyr Glu Gln Tyr Gln
                140                 145                 150

ccg ctg ggc atc gtc ggc atc atc tcg gcc ttc aac ttc ccg gtc gcg        3355
Pro Leu Gly Ile Val Gly Ile Ile Ser Ala Phe Asn Phe Pro Val Ala
                155                 160                 165

gtc tgg gcc tgg aac agc ttc ctg gcc gcg atc tgt ggt gat gtc tgc        3403
Val Trp Ala Trp Asn Ser Phe Leu Ala Ala Ile Cys Gly Asp Val Cys
            170                 175                 180

atc tgg aag ccg tcc aac aag acc ccg ctg acc gcg atc gcg tcc atg        3451
Ile Trp Lys Pro Ser Asn Lys Thr Pro Leu Thr Ala Ile Ala Ser Met
        185                 190                 195

cgc atc tgc aac gaa gca ctg cgc gaa ggc ggc ttc ccg gac atc ttc        3499
Arg Ile Cys Asn Glu Ala Leu Arg Glu Gly Gly Phe Pro Asp Ile Phe
200                 205                 210                 215

ttc ctg atc aac gac gcc ggc acc gcg ttg tcg gag aag ctg gtc gag        3547
Phe Leu Ile Asn Asp Ala Gly Thr Ala Leu Ser Glu Lys Leu Val Glu
                220                 225                 230

gac aag cgc gtg ccg ctg atc tcc ttc acc ggc tcg acc cag gtc ggg        3595
Asp Lys Arg Val Pro Leu Ile Ser Phe Thr Gly Ser Thr Gln Val Gly
                235                 240                 245
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9

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cgc atc gtc aac cag aag gtc gcc gcc cgc ctg ggc cgc tgc ctg ctc     3643
Arg Ile Val Asn Gln Lys Val Ala Ala Arg Leu Gly Arg Cys Leu Leu
        250             255             260

gag ctg ggc ggc aac aac gcg atc atc ctg gac gaa acc gcc gac ctg     3691
Glu Leu Gly Gly Asn Asn Ala Ile Ile Leu Asp Glu Thr Ala Asp Leu
        265             270             275

aag ctg gcc gtg ccg ggc atc gtc ttc ggc gcc gtc ggc acc gcc ggc     3739
Lys Leu Ala Val Pro Gly Ile Val Phe Gly Ala Val Gly Thr Ala Gly
280             285             290             295

cag cgc tgc acc acc acc cgc cgc ctg atc gtg cac gaa tcg atc tac     3787
Gln Arg Cys Thr Thr Thr Arg Arg Leu Ile Val His Glu Ser Ile Tyr
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gac aac gtg ctg gcc acc ttg atc aag gcc tac aag cag gtc gaa ggc     3835
Asp Asn Val Leu Ala Thr Leu Ile Lys Ala Tyr Lys Gln Val Glu Gly
            315             320             325

aag atc ggc gat ccg ctg gat gcc gcc aac ctg atg ggc ccg ctc aac     3883
Lys Ile Gly Asp Pro Leu Asp Ala Ala Asn Leu Met Gly Pro Leu Asn
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agc ccc gaa gcg gtg cag cag ttc ctg gcc tcg atc gag aaa gcc aag     3931
Ser Pro Glu Ala Val Gln Gln Phe Leu Ala Ser Ile Glu Lys Ala Lys
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gcc gct ggc ggc acc gtt caa acc ggt ggt acc gcg atc gac cgc ccg     3979
Ala Ala Gly Gly Thr Val Gln Thr Gly Gly Thr Ala Ile Asp Arg Pro
360             365             370             375

ggc aac ttc gtg ctg ccg gcc atc gtc acc ggc ctg aag aac agc gat     4027
Gly Asn Phe Val Leu Pro Ala Ile Val Thr Gly Leu Lys Asn Ser Asp
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Glu Val Val Gln His Glu Thr Phe Ala Pro Ile Leu Tyr Val Met Lys
            395             400             405
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10

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ggc ctg tcc tcg tcg atc ttc acc acg aac ctg aag gca gcc gag aag   4171
Gly Leu Ser Ser Ser Ile Phe Thr Thr Asn Leu Lys Ala Ala Glu Lys
    425             430                 435

ttc ctg tcg gcg gcc ggc agc gac tgc ggc att gcc aac gtc aac atc   4219
Phe Leu Ser Ala Ala Gly Ser Asp Cys Gly Ile Ala Asn Val Asn Ile
440             445                 450                 455

ggc act tcc ggt gcc gag atc ggc ggc gcc ttc ggt ggc gag aag gaa   4267
Gly Thr Ser Gly Ala Glu Ile Gly Gly Ala Phe Gly Gly Glu Lys Glu
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acc ggc ggt ggc cgt gag tcc ggc tcg gat gcg tgg aag gtc tac atg   4315
Thr Gly Gly Gly Arg Glu Ser Gly Ser Asp Ala Trp Lys Val Tyr Met
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Arg Arg Gln Thr Asn Thr Ile Asn Tyr Ser Asp Ser Leu Pro Leu Ala
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cag ggc atc aag ttc gac ctg taa gccgctcgcc acggcccgcc ttccccggaa   4417
Gln Gly Ile Lys Phe Asp Leu Stop
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<223> Description of Artificial Sequence: Synthesized
      considering the base sequence of a PCR
      amplification fragment of about 400 bp obtained
      based on the N-terminus amino acid sequence
      information using LAPCR in vitro cloning KIT

<400> 4
aaggttttcg acaaagtgac catttccca   29

<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
considering sequences obtained by converting the
PstI sites of base 545 and base 2658 of Sequence
table: 1 to PstI and SacI sites, respectively

<400> 5
ctggtaccgc tcgatccggc tctgcaccgt   30

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
considering sequences obtained by converting the
PstI sites of base 545 and base 2658 of Sequence
table: 1 to PstI and SacI sites, respectively

<400> 6
ctggagctca ggcaggtgcg ggccacgtgt   30